

GenCore version 4.5
Copyright (c) 1993 - 2000 CompuGen Ltd.

OM nucleic - nucleic search, using sw model

Run on: August 27, 2001, 14:25:52 ; Search time 2462.53 Seconds
(without alignments)
1738.920 Million cell updates/sec

Title: US-09-784-340-3_COPY_18322_18774

Perfect score: 453
Sequence: 1 gtaagtactactgtgtgtac.....tgtgtgttttccttcacg 453

Scoring table: IDENTITY_NUC
Gapop 10.0 , Gapext 1.0

Searched: 10228115 seqs, 4726426750 residues

Total number of hits satisfying chosen parameters: 20456230

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Database :

EST:*

1: gb_est1:*
2: gb_est2:*
3: gb_est3:*
4: gb_est4:*
5: gb_est5:*
6: gb_est6:*
7: gb_est7:*
8: gb_est8:*
9: gb_est9:*
10: gb_est10:*
11: gb_est11:*
12: gb_est12:*
13: gb_est13:*
14: gb_est14:*
15: gb_est15:*
16: gb_est16:*
17: gb_est17:*
18: gb_est18:*
19: gb_est19:*
20: gb_est20:*
21: gb_est21:*
22: gb_est22:*
23: gb_est23:*
24: gb_est24:*
25: gb_est25:*
26: gb_est26:*
27: gb_est27:*
28: gb_est28:*
29: gb_est29:*
30: gb_est30:*
31: gb_est31:*
32: gb_est32:*
33: gb_est33:*
34: gb_est34:*
35: gb_est35:*
36: gb_est36:*
37: gb_est37:*
38: gb_est38:*
39: gb_est39:*
40: gb_est40:*
41: gb_est41:*
42: gb_est42:*
43: gb_est43:*

44: em_esthum10:*
45: em_esthum11:*
46: em_esthum12:*
47: em_esthum13:*
48: em_esthum14:*
49: em_esthum15:*
50: em_esthum16:*
51: em_esthum17:*
52: em_esthum18:*
53: em_esthum19:*
54: em_esthum20:*
55: em_esthum21:*
56: em_esthum22:*
57: em_esthum23:*
58: em_esthum24:*
59: em_esthum25:*
60: em_esthum26:*
61: em_esthum27:*
62: em_esthum28:*
63: em_esthum29:*
64: em_esthum30:*
65: em_esthum31:*
66: em_esthum32:*
67: em_esthum33:*
68: em_esthum34:*
69: em_esthum35:*
70: em_esthum36:*
71: em_esthum37:*
72: em_esthum38:*
73: em_esthum39:*
74: em_esthum40:*
75: em_esthum41:*
76: em_esthum42:*
77: em_esthum43:*
78: em_esthum44:*
79: em_esthum45:*
80: em_esthum46:*
81: em_esthum47:*
82: em_esthum48:*
83: em_esthum49:*
84: em_esthum50:*
85: em_esthum51:*
86: em_esthum52:*
87: em_esthum53:*
88: em_esthum54:*
89: em_esthum55:*
90: em_esthum56:*
91: em_esthum57:*
92: em_esthum58:*
93: em_esthum59:*
94: em_esthum60:*
95: em_esthum61:*
96: em_esthum62:*
97: em_esthum63:*
98: em_esthum64:*
99: em_esthum65:*
100: em_esthum66:*
101: em_esthum67:*
102: em_esthum68:*
103: em_esthum69:*
104: em_esthum70:*
105: em_esthum71:*
106: em_esthum72:*
107: em_esthum73:*
108: em_esthum74:*
109: em_esthum75:*
110: em_esthum76:*
111: em_esthum77:*
112: em_esthum78:*
113: em_esthum79:*
114: em_esthum80:*
115: em_esthum81:*
116: em_esthum82:*

117: gb_est48:*
118: gb_est49:*
119: gb_est50:*
120: gb_est51:*
121: gb_est52:*
122: gb_est53:*
123: gb_est54:*
124: gb_est55:*
125: gb_est56:*
126: gb_est57:*
127: gb_est58:*
128: gb_est59:*
129: gb_est60:*
130: gb_est61:*
131: gb_est62:*
132: gb_est63:*
133: gb_est64:*
134: gb_est65:*
135: gb_est66:*
136: gb_est67:*
137: gb_est68:*
138: gb_est69:*
139: gb_est70:*
140: gb_est71:*
141: gb_est72:*
142: gb_est73:*
143: gb_est74:*
144: gb_est75:*
145: gb_est76:*
146: gb_est77:*
147: gb_est78:*
148: gb_est79:*
149: gb_est80:*
150: gb_est81:*
151: gb_est82:*
152: gb_est83:*
153: gb_est84:*
154: gb_est85:*
155: gb_est86:*
156: gb_est87:*
157: gb_est88:*
158: gb_est89:*
159: gb_est90:*
160: gb_est91:*
161: gb_est92:*
162: gb_est93:*
163: gb_est94:*
164: gb_est95:*
165: gb_est96:*
166: gb_est97:*
167: gb_est98:*
168: gb_est99:*
169: gb_est100:*
170: gb_est101:*
171: gb_est102:*
172: gb_est103:*
173: gb_est104:*
174: gb_est105:*
175: gb_est106:*
176: gb_est107:*
177: gb_est108:*
178: gb_est109:*

190: gb_est110:*
191: gb_est111:*
192: gb_hlc:*
193: em_gss_fun:*
194: em_gss_hum1:*
195: em_gss_hum2:*
196: em_gss_hum3:*
197: em_gss_hum4:*
198: em_gss_hum5:*
199: em_gss_hum6:*
200: em_gss_hum7:*
201: em_gss_hum8:*
202: em_gss_hum9:*
203: em_gss_inv1:*
204: em_gss_inv2:*
205: em_gss_inv3:*
206: em_gss_inv4:*
207: em_gss_inv5:*
208: em_gss_inv6:*
209: em_gss_inv7:*
210: em_gss_inv8:*
211: em_gss_inv9:*
212: em_gss_inv10:*
213: em_gss_inv11:*
214: em_gss_inv12:*
215: em_gss_inv13:*
216: em_gss_inv14:*
217: em_gss_inv15:*
218: em_gss_inv16:*
219: em_gss_inv17:*
220: em_gss_inv18:*
221: em_gss_inv19:*
222: em_gss_inv20:*
223: em_gss_inv21:*
224: em_gss_inv22:*
225: em_gss_inv23:*
226: em_gss_inv24:*
227: em_gss_inv25:*
228: em_gss_inv26:*
229: em_gss_inv27:*
230: em_gss_inv28:*
231: em_gss_inv29:*
232: em_gss_inv30:*
233: em_gss_inv31:*
234: em_gss_inv32:*
235: em_gss_inv33:*
236: em_gss_inv34:*
237: em_gss_inv35:*
238: em_gss_inv36:*
239: em_gss_inv37:*
240: em_gss_inv38:*
241: em_gss_inv39:*
242: em_gss_inv40:*
243: em_gss_inv41:*
244: em_gss_inv42:*
245: em_gss_inv43:*
246: em_gss_inv44:*
247: em_gss_inv45:*
248: em_gss_inv46:*
249: em_gss_inv47:*
250: em_gss_inv48:*
251: em_gss_inv49:*
252: em_gss_inv50:*
253: em_gss_inv51:*
254: em_gss_inv52:*
255: em_gss_inv53:*
256: em_gss_inv54:*
257: em_gss_inv55:*
258: em_gss_inv56:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

| Result | Score | Query | Length | DB | ID | Description |
|--------|-------|-------|--------|-----|-----------|---------------------|
| No. | Match | | | | | |
| C 1 | 395.8 | 87.4 | 429 | 225 | A0173790 | A0173790 HS_3194_A |
| C 2 | 318.8 | 70.4 | 407 | 233 | A0805851 | A0805851 HS_3192_A |
| C 3 | 289 | 63.8 | 402 | 257 | B87784 | B87784 RPTc11-3062 |
| C 4 | 233 | 51.4 | 444 | 257 | B80712 | B80712 C1T-HSP-205 |
| C 5 | 130.8 | 28.9 | 335 | 224 | A0106323 | A0106323 HS_3056_A |
| C 6 | 57.4 | 12.7 | 335 | 224 | CNS00396 | AL063921 Drosophill |
| C 7 | 52.6 | 11.6 | 1101 | 219 | CNS016L1 | AL106886 Drosophill |
| C 8 | 52.2 | 11.5 | 1101 | 219 | CNS00738 | AL060732 Drosophill |
| C 9 | 50 | 11.0 | 1101 | 219 | CNS00238 | AL097166 Drosophill |
| C 10 | 49 | 10.8 | 883 | 106 | AL575329 | AL575329 Drosophill |
| C 11 | 48.6 | 10.7 | 1101 | 219 | CNS0106X | AL098595 Drosophill |
| C 12 | 48.4 | 10.7 | 587 | 221 | CNS0440Z | AL281276 Tetraodon |
| C 13 | 48.2 | 10.6 | 843 | 219 | CNS00C51 | AL059666 Drosophill |
| C 14 | 48.2 | 10.6 | 1101 | 219 | CNS0182P | AL108811 Drosophill |
| C 15 | 48 | 10.6 | 1101 | 219 | CNS017YX | AL108676 Drosophill |
| C 16 | 47.8 | 10.6 | 417 | 225 | A0173773 | A0173773 HS_3194_A |
| C 17 | 47.6 | 10.5 | 1201 | 219 | CNS0167M | AL106396 Drosophill |
| C 18 | 46.8 | 10.3 | 624 | 226 | A0291087 | A0291087 rbxpb0038A |
| C 19 | 46.8 | 10.3 | 996 | 219 | CNS00F0H | AL071063 Drosophill |
| C 20 | 46.6 | 10.3 | 911 | 219 | CNS00372 | AL069051 Drosophill |
| C 21 | 46.4 | 10.2 | 847 | 235 | A0900572 | A0900572 HS_3168_B |
| C 22 | 46.4 | 10.2 | 936 | 245 | AZ536291 | AZ536291 ENTC141TF |
| C 23 | 46 | 10.2 | 916 | 219 | CNS006TQ | AL065906 Drosophill |
| C 24 | 45.8 | 10.1 | 916 | 245 | AZ541074 | AZ541074 ENTER58TR |
| C 25 | 45.6 | 10.1 | 1101 | 219 | CNS000B8 | AL063632 Drosophill |
| C 26 | 45.2 | 10.0 | 1101 | 219 | CNS00EVL | AL069706 Drosophill |
| C 27 | 45.2 | 10.0 | 1101 | 222 | CNS05C24 | AL313753 Tetraodon |
| C 28 | 44.8 | 9.9 | 840 | 219 | CNS010TW | AL099422 Drosophill |
| C 29 | 44.8 | 9.9 | 868 | 247 | AZ679258 | AZ679258 ENTV01TFE |
| C 30 | 44.8 | 9.9 | 1101 | 219 | CNS00390 | AL063931 Drosophill |
| C 31 | 44.6 | 9.8 | 1101 | 219 | CNS0006T | AL062049 Drosophill |
| C 32 | 44.2 | 9.8 | 1101 | 219 | CNS00E0Z | AL069440 Drosophill |
| C 33 | 44.2 | 9.8 | 1101 | 219 | CNS00DEP | AL069443 Drosophill |
| C 34 | 44 | 9.7 | 1101 | 219 | CNS00DEO | AL069440 Drosophill |
| C 35 | 43.8 | 9.7 | 784 | 221 | CNS043VT | AL273314 Tetraodon |
| C 36 | 43.6 | 9.6 | 928 | 219 | CNS00DKY | AL071865 Drosophill |
| C 37 | 43.6 | 9.6 | 1009 | 219 | CNS00587 | AL057153 Drosophill |
| C 38 | 43.4 | 9.6 | 779 | 104 | AL1883937 | AL1883937 w25H05.x |
| C 39 | 43.4 | 9.6 | 1001 | 219 | CNS0064G | AL062781 Drosophill |
| C 40 | 43.4 | 9.6 | 1092 | 220 | CNS020K7 | AL175656 Tetraodon |
| C 41 | 43.4 | 9.6 | 1201 | 219 | CNS016CO | AL106578 Drosophill |
| C 42 | 43.4 | 9.6 | 1201 | 219 | CNS016AD | AL106495 Drosophill |
| C 43 | 43.2 | 9.5 | 302 | 15 | AL050897 | AL050897 osw3106.s |
| C 44 | 43.2 | 9.5 | 419 | 165 | BE244937 | BE244937 TCBAR1D26 |
| C 45 | 43.2 | 9.5 | 517 | 20 | AL431788 | AL431788 t125c04.x |

ALIGNMENTS

| Journal MEDLINE COMMENT | scanning the human genome Proc. Natl. Acad. Sci. U. S. A. 96 (17), 9739-9744 (1999) 99380589 Contact: Mahairas GG, Wallace JC, Hood L High Throughput Sequencing Center University of Washington 401 Queen Anne Avenue North, Seattle, WA 98109, USA Tel: (206) 616-3618 Fax: (206) 616-3887 Email: jwallace@u.washington.edu Sequence Tagged Connector Plate: 3194 row: 0 column: 9 Class: BAC ends High quality sequence stop: 429. |
|-------------------------------|--|
| FEATURES | Location/Qualifiers |
| source | 1. .429 /organism="Homo sapiens" /db_xref="taxon:9606" /clone="Plate-3194 Col-9 Row 1" /clone_lib="CTR Approved Human Genomic Sperm Library D" /sex="male" /note="Organ: sperm; Vector: pBelBAC11; BAC Clones in E-Coli DH10B" |
| BASE COUNT | 159 a 61 c 77 g 132 t. |
| ORIGIN | |
| Query Match | 87.4%; Score 395.8; D: 225; Length 429; |
| Best Local Similarity | 99.5%; Pred. No. 7.7e-4; |
| Matches 397; Conservative | 0; Mismatches 2; Indels 0; Gaps 0; |
| QY | 55 accagaaaatgttaataatcattccctcgtgagacatgttga;attttctccacaattt 114 |
| Db | 428 ACCAAGAGATGTTAAATATCATCCGGTAGAGATATTTGAGAGATTTCACCAATAT 369 |
| QY | 115 gattcatccatcacctgttacctggaatagttgtgaa;gtagttcatagatgtcaa 174 |
| Db | 368 GAGTATTCATCACCTTGTGTACTGGAATAGTTGTGAAATGTAGTTCTATAGTGTCGA 309 |
| QY | 175 acctctccatggaatatataggtttaagttaaagtaaacatg;ttactaaagctttatcac 234 |
| Db | 308 ACTTCTTCATGAGATATTAGTTTAAAGTTAAACAACGCTTTACTAAGCTTTTATTCAC 249 |
| QY | 235 attctaatttaaccattttgtttaagaatatataccttt;ttctctcacatatatcgt 294 |
| Db | 248 ATCTTAATTTTACCCCATTTTGTATAGAATATATCTTTTGGTCTCCACATATATCT 189 |
| QY | 295 ttaatactatgtaaacacaatatcatatgtaacacacagct;caatcttttactgaacat 354 |
| Db | 168 TTAATACATATGTAACCAACAATATTCATGTCCACACCAATTCATATCTTTACTGAAC 129 |

RESULT 4
LOCUS B80712
DEFINITION CIT-HSP-2050M23.TR CIT-HSP Homo sapiens genomic clone 2050M23. DNA
SEQUENCE.
ACCESSION B80712
VERSION B80712
KEYWORDS GI:2867735
SOURCE GSS.
ORGANISM human.
REFERENCE Homo sapiens
AUTHORS Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominiidae; Homo.
1 (bases 1 to 444)
Adams,M.D., Rounsley,S.D., Zhao,S., Field,C.E., Baas,S., Linher,K.,
Simon,M., and Venter,J.C.
Golden,K., Berry,K., Granger,D., Suh,E., Wible,C., Shizuya,H.,
Use of a random BAC End Sequence Database for Sequence-Ready Map
Building (1998)
Unpublished (1998)
Other_GSS: CIT-HSP-2050M23.TR
JOURNAL COMMENT
Contact: Mark Adams
Department of Eukaryotic Genomics
The Institute for Genomic Research
9712 Medical Center Dr., Rockville, MD 20850, USA
Tel: 301 838 0200
Fax: 301 838 0208
Email: mdamas@tigr.org
Clones are available from Research Genetics (info@resgen.com). BAC
end search page:
http://www.tigr.org/cdb/humgen/bac_end_search/bac_end_search.html
Seq primer: M13-21
Class: BAC ends.

FEATURES
source
Location/Qualifiers
1..444
/organism="Homo sapiens"
/db_xref="GDB:7056598"
/db_xref="taxon:9606"
/clone="2050M23"
/clone_1ib="CIT-HSP"
/sex="Male"
/cell_type="Sperm"
/note="Vector: pBelBAC11; site_1: HindIII; site_2:
HindIII"

BASE COUNT 124 a 110 c 71 g 139 t
ORIGIN

Query Match 51.4%; Score 233; DB 257; Length 444;
Best Local Similarity 100.0%; Pred. No. 3.6e-44;
Matches 233; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 221 aagctttattacatcttaatttaccacatttgttaagaatatactcttcaagtc 280
|||||
DB 54 AACCTTTATTCACATCTTAATTTTACCCCATTTTGTAGAAATATCTCTTCAGTCTC 113
|||||

QY 281 tccacatatactgttaataactatgttaaccaataatctatgtcaacaaccagaatcaat 340
|||||
DB 114 TCCACATATCTGTTAAATCTATGTAAACCAACAATTTTATGTCACAAACAGATCAAT 173
|||||

QY 341 cttctactgaacatgtcttgcgttcgacataacatactacggtttactacgtctctt 400
|||||
DB 174 CTTTACTGACACATGTTCTTGCGCTTGCAATATACATATCTACGAGTTATCTTACGTTCTTT 233
|||||

QY 401 tatgaaacaaactacaactcttcaagttcatalgtlgtlgtttccctccag.453
|||||
DB 234 TATGAAACAAACTACAACTTCTTAAGTCTATGTGTGTTTCCCTTCAG 286
|||||

RESULT 5
LOCUS AQ106323/c 335 bp DNA GSS 28-AUG-1998
DEFINITION HS_3056_A2_D08_MF CIT Approved Human Genomic Sperm Library D Homo

ACCESSION sapiens genomic clone Plate=3056 Col=16 Row=G, DNA sequence.
AQ106323
LOCUS AQ106323.1 GI:3481679
KEYWORDS GSS.
SOURCE human.
ORGANISM Homo sapiens
REFERENCE Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominiidae; Homo.
1 (bases 1 to 335)
Mahairas,G.G., Wallace,J.C., Smith,K., Swartzell,S., Holzman,T.,
Keller,A., Shaker,R., Furlong,J., Young,D., Zhao,S., Adams,M.D., and
Hood,L.
Sequence-tagged connectors: A sequence approach to mapping and
scanning the human genome
Proc. Natl. Acad. Sci. U. S. A. 96 (17), 9739-9744 (1999)
JOURNAL MEDLINE
99380589
COMMENT Contact: Mahairas GG, Wallace JC, Hood L
High Throughput Sequencing Center
University of Washington
401 Queen Anne Avenue North, Seattle, WA 98109, USA
Tel: (206) 616-3618
Fax: (206) 616-3887
Email: jwallace@u.washington.edu
Sequence Tagged Connector
Plate: 3056 row: G column: 16
Class: BAC ends
High quality sequence stop: 335.

FEATURES
source
Location/Qualifiers
1..335
/organism="Homo sapiens"
/db_xref="taxon:9606"
/clone="Plate=3056 Col=16 Row=3"
/clone_1ib="CIT Approved Human Genomic Sperm Library D"
/sex="male"
/note="Organ: sperm; Vector: pBelBAC11; BAC Clones in
E-Coli DH10B"

BASE COUNT 113 a 50 c 69 g 103 t
ORIGIN

Query Match 28.9%; Score 130.8; DB 224; Length 335;
Best Local Similarity 69.5%; Pred. No. 1.6e-20;
Matches 221; Conservative 0; Mismatches 12; Indels 5; Gaps 3;

QY 30 taacattgactaagtattacattataccagaagaatgttaa:atcatccggttagaatg 89
|||||
DB 315 TACCATGAGTATGTTATTA-ATCATCTAGAGATGTCAG-3GCCATPACATGAGACTAT 257
|||||

QY 90 ttgaggatttactccacaatataggatcatcatcacc:tgtagtgaatagtgtg 149
|||||
DB 256 ATAAAGATATTCGCCCTCAATTCACAGTCAATTTATATATC TACCATTGCA--AGTCTG 199
|||||

QY 150 gaaattgatlcatagagtgltcaaatcttcttcataagaa:attaggtttaagttaaca 209
|||||
DB 198 GAAATGTAATGATAGAGTCAATCTCTTCTTGAA:ACTAGATTTAAATTAAGG 139
|||||

QY 210 acggtctactaagctttatcatcattcaatttcccatl--tgttaagaataata 267
|||||
DB 138 ACCAGCTTACTAAGTATTTTCTATGCTCATTTTACCCT:TTGTGATTAAGAAATATCTT 79
|||||

QY 268 ctctttagctctccacatatactgtttaataactatgtt:ccaacaataactatgtcac 327
|||||
DB 78 CTTTITTAATTTGCCCTGCTAGCTCTTACGTGATATGCA:TCACAAAGATTATATATCAC 19
|||||

QY 328 aaccagaatcaatcttt 345
|||||
DB 18 AACAAAGATCTATCTTT 1
|||||

RESULT 6
LOCUS CNS0039G 1101 bp DNA GSS 03-JUN-1999
DEFINITION Drosophila melanogaster genome survey sequence TET3 end of BAC #

| RESULT | 9 |
|------------|---|
| CNS00Z38/c | |
| LOCUS | CNS00Z38 1101 bp DNA GSS 26-JUL-1999 |
| DEFINITION | Drosophila melanogaster genome survey sequence SP6 end of BAC |

| | | | | |
|------------|--|-------------|------|-------------|
| RESULT | 10 | | i | |
| AL575329 | | | | |
| LOCUS | AL575329 | 883 bp | mRNA | EST |
| DEFINITION | AL575329 LTI_NFL006_PL2 Homo sapiens cDNA clone CS0D1061YP18 3 prime, mRNA sequence. | | | 16-FEB-2001 |
| ACCESSION | AL575329 | | | |
| VERSION | AL575329.1 | GI:12936390 | | |
| KEYWORDS | EST. | | | |
| SOURCE | human. | | | |
| ORGANISM | Homo sapiens | | | |
| | Eumetazoa; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi | | | |
| | Mammalia; Euthera; Primates; Catarrhini; Homnidae; Homo. | | | |

melanogaster genome using these BACs. For further information please see <http://www.fruitfly.org> The BDGP Drosophila melanogaster BAC library was prepared by Kazutoyo Oseegawa and Aaron Mammosser in Pieter de Jong's laboratory in the Department of Cancer Genetics at the Roswell Park Cancer Institute in Buffalo, NY. The library is named RPCI-98 and was constructed by partial EcoRI digestion of Drosophila DNA provided by the BDGP from the isogenic strain y2; cn bw sp. the same strain used for the library p1 and EST libraries. A more detailed description of the library and how to order individual BAC clones, the entire library, or filters for hybridization from the BACPAC Resource Center can be found at http://bacpac.med.buffalo.edu/drosophila_bac.htm.

collaboration with the European Drosophila Genome Project (EDGP) - <http://www.edgp.ebi.ac.uk> - This Drosophila melanogaster BAC library (Dros BAC) was made by Alain Billand at CEPH (Centre d'Etude du Polymorphisme Humain) with funding provided by a MRC project grant. The DNA was prepared from embryos by Alain Bucheton and Genevieve Payan. It has been constructed in the vector pBelobAC11.

FEATURES
source 1. 1101
/organism="Drosophila melanogaster"
/plasmid="pBelobAC11"
/db_xref="taxon:7227"
/clone_1ib="DrosBAC"
/clone="BACN37D10"
/note="end : SP6"

BASE COUNT 274 a 268 c 128 g 73 t 358 others
ORIGIN

Query Match 10.6%; Score 48.2; DB 219; Length 1101;
Best Local Similarity 20.5%; Pred. No. 0.21;
Matches 89; Conservative 167; Mismatches 178; Indels 1; Gaps 1;

```

OY 11 ctcgtgtacacagatgataacatgataatgataacataacagaagaatgtaa 70
Db 1057 MYNNHTAAUHMCHNHNHUTWHTGWTGCMYUAMUCYUCSNHMMHMAUAMMMHMYUAMA 998
OY 71 tctacatcctgtagacatgttgagggatcttaacatcaaatatgagcatcacaact 130
Db 997 MNNHNNHMMSCAMSMHMYUAMHMMSCCMHMMHNNHTATGHTNHYUHMWCHTMT 938
OY 131 tctactgataatgtagtgaa-attgtagtcatagatgtagaactcttcacagaa 189
Db 937 TMMNHTMNNHNNHNNHMAAAMHNNATGTWNNMANNHTTUTTTTTTTTTTTTTTTTTT 878
OY 190 atataagtgtaagtaacacagatgataacatgataacatccttaactacac 249
Db 877 TTTTNNHMTTAAHNNHMYUAMHNNHMMHMYUAMWMAAMTTTTTTTTTTTTTTTTTTTT 818
OY 250 cacttctgtaagaataactcttcagctctcacaataatcgttctaactatgaac 309
Db 817 TTTTTCCTTTCCTTTCCTTTCCTTTCCTTTCCTTTCCTTTCCTTTCCTTTCCTTTCCTT 758
OY 310 caacaatactgatacacaacagaataactcttaacagatactgtagatgtagat 369
Db 757 TTMAMTATACNNHMTGTTTATATGSCNNHMMHMMHMMHMMHMMHMMHMMHMMHMMHMM 698
OY 370 aacatactacagttatcagttccttcttaagaacaacaacatacacttcaagt 429
Db 697 TMTHTTTTTTTTTTTTTTTCCTTTCCTTTCCTTTCCTTTCCTTTCCTTTCCTTTCCTT 638
OY 430 tctatgtagtctttt 444
Db 637 ACTTTTTTTTTTTTTT 623

```

RESULT 15
CNS017YY/c 1101 bp DNA GSS 26-JUL-1999
LOCUS Drosophila melanogaster genome survey sequence T7 end of BAC
DEFINITION BACN37B08 of DrosBAC library from Drosophila melanogaster (fruit
fly), genomic survey sequence.

ACCESSION AL108676.1 GI:5628980

VERSION AL108676

KEYWORDS GSS.

SOURCE fruit fly.

ORGANISM Plasmid Drosophila melanogaster

Eukaryota; Metazoa; Arthropoda; Tracheata; Hexapoda; Insecta;

Pterygota; Neoptera; Endopterygota; Diptera; Brachycera;

Muscomorpha; Ephydroidea; Drosophilidae; Drosophila.

REFERENCE 1 (bases 1 to 1101)

AUTHORS Genoscope.

TITLE Direct Submission

JOURNAL

Submitted (23-JUL-1999) Genoscope - Centre National de Sequencage :
BP 91 91006 EVRY cedex - FRANCE (E-mail : seqref@genoscope.cns.fr)
- Web : www.genoscope.cns.fr
COMMENT
determination of this BAC-end sequence was carried out as part of a
collaboration with the European Drosophila Genome Project (EDGP) -
<http://www.edgp.ebi.ac.uk> - This Drosophila melanogaster BAC
library (Dros BAC) was made by Alain Billand at CEPH (Centre
d'Etude du Polymorphisme Humain) with funding provided by a MRC
project grant. The DNA was prepared from embryos by Alain Bucheton
and Genevieve Payan. It has been constructed in the vector
pBelobAC11.

FEATURES
source 1. 1101
/organism="Drosophila melanogaster"
/plasmid="pBelobAC11"
/db_xref="taxon:7227"
/clone_1ib="DrosBAC"
/clone="BACN37B08"
/note="end : T7"

BASE COUNT 363 a 143 c 158 g 215 t 222 others
ORIGIN

Query Match 10.6%; Score 48; DB 219; Length 1101;
Best Local Similarity 30.2%; Pred. No. 0.24;
Matches 124; Conservative 94; Mismatches 112; Indels 1; Gaps 1;

```

OY 39 ctatgtataacattacacagaagaatgtaaatcaccatgtagacatgttgagggat 98
Db 1059 CTTTCTTTTCTTTTCTTTTCTTTTCTTTTCTTTTCTTTTCTTTTCTTTTCTTTTCTTT 1000
OY 99 tttacacacacatagatgatacctccttgtagcgaatgtagttagttagttagt 158
Db 999 WTATGTCATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGAT 940
OY 159 gtcatagatgtaacatcttcacatgtaaatatagatgaatgaacacagtgct 218
Db 939 UATGACATGTTGTCGTCGTCGTCGTCGTCGTCGTCGTCGTCGTCGTCGTCGTCGTCGTCG 880
OY 219 ctatgcttctatcacaacttaatttaacccatcttgcttagaataactcttca 278
Db 879 AAATATTTTTTTTTCAMNNHMMHMMHMMHMMHMMHMMHMMHMMHMMHMMHMMHMM 820
OY 279 tctcactatctgcttatactatgtaacacacatatcatgtaacacacacac 338
Db 819 TTTMMMAV-THTTTTACCAATGTTTTCMCMHMMHMMHMMHMMHMMHMMHMMHMMHMMH 761
OY 339 atccttaacagacatgcttcctgctgataacacatactacagttatcagtgct 398
Db 760 ATGACCTMTTAAATGTTTAAATGATGACAAATATGTTTACTTTTCTTTTCTTTTCTTT 701
OY 399 ttatgaacaacaacatacacttcttaagttcatagttgctttctccctt 449
Db 700 MAMHAAAMMMHMAAAATGAMHTATTTTTTTTTTTTTTTTCTTTTCTTTTCTTTTCTTTT 650

```

Search completed: August 27, 2001, 17:07:35
Job time: 9703 sec

This Page Blank (uspto)